

**IN THE UNITED STATES DISTRICT COURT
FOR THE NORTHERN DISTRICT OF OHIO**

CYBERGENETICS CORP.,

Plaintiff,

v.

INSTITUTE OF ENVIRONMENTAL SCIENCE
AND RESEARCH and NICHEVISION INC.,

Defendants.

Case No. _____

JURY TRIAL DEMANDED

COMPLAINT FOR PATENT INFRINGEMENT

Plaintiff Cybergenetics Corp. (“Cybergenetics”) hereby asserts a claim for patent infringement against Defendants the Institute of Environmental Science and Research (“ESR”) and NicheVision Inc. (“NicheVision”) (collectively, “Defendants”), and in support thereof alleges, based on actual knowledge as to Cybergenetics’ own activities and on information and belief as to the activities of others, as follows:

Nature of the Action

1. This is an action for patent infringement arising under the patent laws of the United States, 35 U.S.C. § 1 *et seq.*, specifically including 35 U.S.C. § 271.

2. As set forth in detail below, ESR and NicheVision have infringed U.S. Patent No. 8,898,021 (“the ’021 Patent”) and U.S. Patent No. 9,708,642 (“the ’642 Patent”) (collectively, “the Patents-in-Suit”), both individually and through their combined actions, in connection with supplying the STRmix™ probabilistic genotyping software product and related services to customers in the United States.

The Parties

3. Cybergenetics Corp. is a corporation organized under the laws of the Commonwealth of Pennsylvania, with its principal place of business at 160 N Craig Street, Suite 210, Pittsburgh, Pennsylvania 15213.

4. On information and belief, the Institute of Environmental Science and Research is a corporation organized and existing under the laws of New Zealand, with a principal place of business at 34 Kenepuru Drive, Kenepuru, Porirua 5022, New Zealand. ESR is a Crown Research Institute of the New Zealand Government.

5. On information and belief, NicheVision Inc. is a corporation organized and existing under the laws of the State of Ohio, with a principal of business at 526 South Main Street, Suite 714G, Akron, Ohio 44311.

Jurisdiction and Venue

6. This Court has subject matter jurisdiction over this patent infringement action pursuant to 28 U.S.C. §§ 1331 and 1338(a).

7. This Court has personal jurisdiction over ESR pursuant to the Ohio Long-arm Statute, Ohio Revised Code § 2307.382, at least because ESR: (i) has transacted business in Ohio, (ii) has contracted to supply services or goods in Ohio, and (iii) has caused tortious injury by an act in Ohio. More particularly, on information and belief, ESR has entered into an agreement with NicheVision pursuant to which NicheVision acts as the exclusive sales representative and distributor of the STRmix™ probabilistic genotyping software product and related services for the entire United States, including Ohio. Through its contractual relationship with NicheVision, ESR has purposefully directed its activities towards Ohio, and thus this Court's exercise of personal jurisdiction over ESR is reasonable and consistent with the requirements of the Due Process Clause of the United States Constitution.

8. This Court has personal jurisdiction over NicheVision by virtue of NicheVision being incorporated in the State of Ohio, maintaining its principal place of business in the State of Ohio, and doing business in the State of Ohio.

9. Venue may lie in this judicial district as to Cybergenetics' claims against ESR pursuant to 28 U.S.C. §§ 1391(c) and/or 1400(b) at least because ESR, as an entity not resident in the United States, may be sued in any judicial district.

10. Venue may lie in this judicial district as to Cybergenetics' claims against NicheVision pursuant to 28 U.S.C. §§ 1391(b)-(d) and/or 1400(b) at least because NicheVision resides in this judicial district, and because a substantial part of the events giving rise to this infringement claim occurred in this judicial district.

11. Joinder of Cybergenetics' claims against ESR and NicheVision is permissible under 35 U.S.C. § 299 because (a) Cybergenetics is seeking to hold Defendants jointly and severally liable for infringement of the Patents-in-Suit, and the claims against each Defendant arise out of the same transaction, occurrence, or series of transactions or occurrences relating to the making, using, importing, offering for sale, or selling of the same accused product, and (b) questions of fact common to all Defendants will arise in this action. More particularly, on information and belief, ESR makes the accused STRmix™ probabilistic genotyping software product in New Zealand, ESR and/or NicheVision import the product into the United States, and ESR and/or NicheVision offer to sell and sell the product to customers in the United States.

The Patents-in-Suit

12. The '021 Patent, titled "Method and System for DNA Mixture Analysis," was duly and legally issued by the United States Patent and Trademark Office on November 25, 2014. The '021 Patent issued from U.S. Patent Application No. 09/776,096 filed February 2,

2001 (“the ’096 Application”). The ’021 Patent will expire on February 2, 2021. A true and correct copy of the ’021 Patent is attached hereto as Exhibit A.

13. The ’642 Patent, titled “Method and System for DNA Mixture Analysis,” was duly and legally issued by the United States Patent and Trademark Office on July 18, 2017. The ’642 Patent issued from U.S. Patent Application No. 14/548,972 filed November 20, 2014 (“the ’972 Application”). The ’972 Application is a continuation of the ’096 Application. The ’642 Patent will expire on February 2, 2021. A true and correct copy of the ’642 Patent is attached hereto as Exhibit B.

14. The Patents-in-Suit are generally directed to computer-based systems and methods for analyzing a DNA sample comprising a mixture of DNA from multiple sources. In accordance with a particular embodiment, the method may comprise the steps of (i) obtaining a mixed DNA sample, (ii) amplifying the DNA sample to produce a product, (iii) detecting the product to produce a signal, and (iv) analyzing the signal to determine information about the composition of the mixed DNA sample.

15. The patented DNA mixture analysis inventions have particular applicability in the field of forensic science, being useful for helping to find and convict criminals, as well as to exonerate innocent suspects, from a sample comprising a mixture of DNA from multiple individuals. A system implementing the inventions can provide high-quality estimates, and can be used to determine genotypes, mixture weights, and likelihood ratios. Such a system provides confidence measures in the results it computes, and can be used to generate reports and intuitive visualizations. Accordingly, the patented inventions can be applied to assist in the identification of a suspect from a mixture of DNA from multiple individuals, thereby greatly improving the effectiveness of DNA crime analysis.

16. Cybergenetics is the owner by assignment of the Patents-in-Suit, having received the entire right, title and interest in and to the inventions covered by the Patents-in-Suit.

COUNT I
Infringement of U.S. Patent No. 8,898,021

17. Cybergenetics incorporates by reference the allegations in Paragraphs 1 through 16 above.

18. Defendants are indirectly infringing the '021 Patent in connection with their licensing, sale and/or distribution of the STRmix™ probabilistic genotyping software to customers in the United States who then use the software to practice methods covered by one or more claims of the patent, in violation of 35 U.S.C. §§ 271(b)-(c). Defendants are also directly infringing the '021 Patent in connection with their own use of the STRmix™ probabilistic genotyping software to practice methods covered by one or more claims of the patent on behalf of customers and/or potential customers in the United States, in violation of 35 U.S.C. §§ 271(a).

19. An example of how use of the STRmix™ probabilistic genotyping software infringes the '021 Patent follows, based on information currently available to Cybergenetics. This example is not intended to limit the scope of Cybergenetics' infringement claim in any way, and is intended to be without prejudice to Cybergenetics' ability to assert different or additional claims of the '021 Patent against Defendants and/or to apply such claims to the accused product differently in view of additional information that Cybergenetics may acquire during the course of the litigation.

20. Claim 1 of the '021 Patent recites as follows:

1. A method of analyzing a DNA mixture comprised of the steps:

(a) obtaining a DNA mixture that contains genetic material from at least two contributing individuals;

(b) amplifying the DNA mixture in a DNA amplification process to produce an amplification product comprising DNA fragments;

(c) producing from the amplification product a signal comprising signal peaks from the DNA fragments;

(d) detecting signal peak amounts in the signal, and quantifying the amounts to produce DNA lengths and concentrations from the mixture to form quantitative genotyping data;

(e) assuming a genotype value of alleles for a contributor to the quantitative genotyping data at a genetic locus;

(f) setting a mixture weight value for a relative proportion of the contributors to the quantitative genotyping data;

(g) forming a linear combination of the genotype values based on the mixture weight value;

(h) deriving with a computer a data variance of the amplification process from a model that includes both the quantitative genotyping data and the linear combination;

(i) determining with the computer a probability of the quantitative genotyping data corresponding to a set of suspects from the DNA mixture at the locus using both the linear combination and the data variance value;

(j) computing a probability of a genotype for one of the contributing individuals using the determined probability of the quantitative genotyping data; and

(k) comparing the genotype probability with a set of suspect genotypes to identify a likely suspect.

'021 Patent at col. 46, ln. 61 – col. 47, ln. 25 (Ex. A). On information and belief, use of the STRmix™ probabilistic genotyping software satisfies each and every limitation of claim 1.

21. With reference to the preamble of claim 1 of the '021 Patent, the STRmix™ probabilistic genotyping software is configured to perform a “method of analyzing a DNA mixture.” *See, e.g.*, STRmix™ Website, <https://www.strmix.com/#what> (last accessed 5/23/19) (Ex. C hereto) (hereinafter, “STRmix™ Website”); D. Taylor *et al.*, “The Interpretation of Single

Source and Mixed DNA Profiles,” *Forensic Sci. Int. Genet.*, Vol. 7, Issue 5, Sept. 2013, 517 (Ex. D hereto) (hereinafter, “Taylor”).

22. With reference to element (a) of claim 1, use of STRmix™ requires, as a necessary precondition, performing the step of “obtaining a DNA mixture that contains genetic material from at least two contributing individuals.” *See, e.g.*, STRmix™ Website; Taylor at 524; STRmix™ Probabilistic Genotyping Software Operating Instructions, ¶¶ 1.1.1-1.1.2 (June 25, 2018) (Ex. E hereto) (hereinafter, “STRmix™ Operating Instructions”).

23. With reference to element (b) of claim 1, use of STRmix™ requires, as a necessary precondition, performing the step of “amplifying the DNA mixture in a DNA amplification process to produce an amplification product comprising DNA fragments.” *See, e.g.*, STRmix™ Operating Instructions at ¶ 1.1.3; Taylor at 524; J. Buckleton *et al.*, Forensic DNA Evidence Interpretation, 3-5 (2nd ed. 2016) (excerpts at Ex. F hereto) (hereinafter, “Buckleton”).

24. With reference to element (c) of claim 1, use of STRmix™ requires, as a necessary precondition, performing the step of “producing from the amplification product a signal comprising signal peaks from the DNA fragments.” *See, e.g.*, STRmix™ Operating Instructions at ¶¶ 1.1.3, 1.1.5; Buckleton at 3-5; Taylor at 524.

25. With reference to element (d) of claim 1, use of STRmix™ requires, as a necessary precondition, performing the step of “detecting signal peak amounts in the signal, and quantifying the amounts to produce DNA lengths and concentrations from the mixture to form quantitative genotyping data.” *See, e.g.*, STRmix™ Operating Instructions at ¶¶ 1.1.3, 1.1.5; Buckleton at 281-86; Taylor at 516-28.

26. With reference to element (e) of claim 1, STRmix™ is used to perform a method that includes the step of “assuming a genotype value of alleles for a contributor to the quantitative genotyping data at a genetic locus.” *See, e.g.*, Buckleton at 295, Fig. 9.10; Taylor at 517-8, 520.

27. With reference to element (f) of claim 1, STRmix™ is used to perform a method that includes the step of “setting a mixture weight value for a relative proportion of the contributors to the quantitative genotyping data.” *See, e.g.*, Buckleton at 281; Taylor at 518, 520; STRmix™ Operating Instructions at ¶ 6.8.2.

28. With reference to element (g) of claim 1, STRmix™ is used to perform a method that includes the step of “forming a linear combination of the genotype values based on the mixture weight value.” *See, e.g.*, Buckleton at Fig. 9.10; Taylor at 518, 520.

29. With reference to element (h) of claim 1, STRmix™ is used to perform a method that includes the step of “deriving with a computer a data variance of the amplification process from a model that includes both the quantitative genotyping data and the linear combination.” *See, e.g.*, Buckleton at 293; Taylor at 518-19, 521.

30. With reference to element (i) of claim 1, STRmix™ is used to perform a method that includes the step of “determining with the computer a probability of the quantitative genotyping data corresponding to a set of suspects from the DNA mixture at the locus using both the linear combination and the data variance value.” *See, e.g.*, STRmix™ Operating Instructions at ¶¶ 6.6-6.7; Buckleton at 293; Taylor at 519.

31. With reference to element (j) of claim 1, STRmix™ is used to perform a method that includes the step of “computing a probability of a genotype for one of the contributing individuals using the determined probability of the quantitative genotyping data.” *See, e.g.*,

STRmix™ Operating Instructions at ¶¶ 2.9-2.10; Buckleton at Fig. 9.11; Taylor at 517, 519-20, 524.

32. With reference to element (k) of claim 1, STRmix™ is used to perform a method that includes the step of “comparing the genotype probability with a set of suspect genotypes to identify a likely suspect.” *See, e.g.*, STRmix™ Website; STRmix™ Operating Instructions at ¶¶ 3-4; Buckleton at 293-94; Taylor at 523; S. Cooper et al., “STRmix: The Application of a Continuous Statistical Model Expert System to Forensic Casework in New Zealand (and Australia),” *Promega ISHI Conference*, 2017, ¶¶ 3, 5 (Ex. G hereto) (hereinafter, “Cooper”).

33. The foregoing element-by-element comparison demonstrates that use of the accused STRmix™ probabilistic genotyping software product on suitable biological input data literally satisfies each and every element of at least claim 1 of the '021 Patent, thus literally infringing the patent. To the extent any element of claim 1 is deemed not to be literally satisfied, use of STRmix™ would nevertheless still infringe under the doctrine of equivalents because any differences between the claimed invention and the method performed by the accused software product are insubstantial.

34. On information and belief, ESR and NicheVision (as ESR's exclusive sales representative) sell and offer to sell the STRmix™ probabilistic genotyping software product to customers in this judicial district and elsewhere in the United States, including numerous state and local law enforcement agencies and forensics laboratories.

35. The STRmix™ probabilistic genotyping software product constitutes a material part of the invention recited in claim 1 of the '021 Patent, being programmed to cause a material and substantial portion of the recited method steps to be performed, and it is not a staple article or commodity of commerce suitable for substantial non-infringing use. Moreover, on

information and belief, Defendants are aware of the '021 Patent at least as a result of communications and interactions between Dr. Mark Perlin, the named inventor on the Patents-in-Suit and a co-founder of Cybergenetics, and Dr. John Buckleton, one of the developers of STRmix™ and a Principal Scientist at ESR. Consequently, Defendants know that the STRmix™ probabilistic genotyping software product is especially made or especially adapted for use in a manner that infringes the '021 Patent. Accordingly, Defendants' sale of the STRmix™ probabilistic genotyping software product contributes to infringement of the '021 Patent by their customers in violation of 35 U.S.C. § 271(c).

36. On information and belief, both by configuring the STRmix™ probabilistic genotyping software product to operate in a manner that Defendants know infringes the '021 Patent, and by encouraging customers to use the STRmix™ probabilistic genotyping software product in a manner that Defendants know infringes the '021 Patent through training, product literature and customer support, Defendants are inducing infringement of the '021 Patent by their customers in violation of 35 U.S.C. § 271(b).

37. Defendants' infringement of the '021 Patent has caused Cybergenetics to suffer substantial monetary harm, including lost profits and price erosion relating to Cybergenetics' sale of competing and related products and services in the same markets served by Defendants.

38. The '021 Patent includes only method claims, and therefore the notice requirements of 35 U.S.C. § 287(a) are inapplicable. Cybergenetics is thus entitled to collect damages for any infringement of the '021 Patent by Defendants occurring up to six (6) years prior to the filing of this complaint in accordance with 35 U.S.C. § 286.

39. Defendants' infringement of the '021 Patent has caused and will continue to cause irreparable harm to Cybergenetics for which there is no adequate remedy at law, including but

not limited to lost market share and lost goodwill that Cybergenetics would otherwise garner as the recognized innovator and sole authorized source of supply for probabilistic genotyping software configured to practice the methods covered by the '021 Patent.

40. On information and belief, Defendants' infringement of the '021 Patent has been willful, done deliberately and with full knowledge that the sale, offer to sell and use of the STRmix™ probabilistic genotyping software product infringes the '021 Patent, and without any reasonable, good-faith belief that the '021 Patent is invalid and/or not infringed, thereby justifying an increase in the damages to be awarded to Cybergenetics by up to three times the amount found or assessed, in accordance with 35 U.S.C. § 284.

41. Defendants' willful infringement of the '021 Patent renders this an exceptional case within the meaning of 35 U.S.C. § 285, justifying an award to Cybergenetics of its reasonable attorney fees incurred in connection with this litigation.

COUNT II
Infringement of U.S. Patent No. 9,708,642

42. Cybergenetics incorporates by reference the allegations in Paragraphs 1 through 16 above.

43. Defendants are indirectly infringing the '642 Patent in connection with their licensing, sale and/or distribution of the STRmix™ probabilistic genotyping software to customers in the United States who then use the software to practice methods covered by one or more claims of the patent, in violation of 35 U.S.C. §§ 271(b)-(c). Defendants are also directly infringing the '642 Patent in connection with their own use of the STRmix™ probabilistic genotyping software to practice methods covered by one or more claims of the patent on behalf of customers and/or potential customers in the United States, in violation of 35 U.S.C. §§ 271(a).

44. An example of how use of the STRmix™ probabilistic genotyping software infringes the '642 Patent follows, based on the information currently available to Cybergenetics. This example is not intended to limit the scope of Cybergenetics' infringement claim in any way, and is intended to be without prejudice to Cybergenetics' ability to assert different or additional claims of the '642 Patent against Defendants and/or to apply such claims to the accused product differently in view of additional information that Cybergenetics may acquire during the course of the litigation.

45. Claim 1 of the '642 Patent recites as follows:

1. A method of analyzing a biological sample comprised of the steps:
 - (a) obtaining a biological sample that contains DNA;
 - (b) amplifying the DNA to produce a product;
 - (c) detecting the product to generate data, where the data can be explained by more than one genotype value;
 - (d) assuming a genotype value which is stored in a nontransient memory;
 - (e) deriving with a computer a variance of the amplification; and
 - (f) determining a likelihood using a computer in communication with the memory, where the likelihood is defined as a probability of observing the generated data, and said probability depends on the genotype value and the variance.

'642 Patent at col. 48, ln. 37-51. On information and belief, use of the STRmix™ probabilistic genotyping software product satisfies each and every limitation of claim 1.

46. With reference to the preamble of claim 1 of the '642 Patent, the STRmix™ probabilistic genotyping software is configured to perform a “method of analyzing a biological sample.” *See, e.g.*, STRmix™ Website; Buckleton at 1-35, 281.

47. With reference to element (a) of claim 1, use of STRmix™ requires, as a necessary precondition, performing the step of “obtaining a biological sample that contains DNA.” *See, e.g.*, STRmix™ Website; STRmix™ Operating Instructions at ¶¶ 1.1.1-1.1.2; Buckleton at 1-3.

48. With reference to element (b) of claim 1, use of STRmix™ requires, as a necessary precondition, performing the step of “amplifying the DNA to produce a product.” *See, e.g.*, STRmix™ Operating Instructions at ¶ 1.1.3; Buckleton at 3-5.

49. With reference to element (c) of claim 1, use of STRmix™ requires, as a necessary precondition, performing the step of “detecting the product to generate data, where the data can be explained by more than one genotype value.” *See, e.g.*, STRmix™ Operating Instructions at ¶¶ 1.1.3, 1.1.5; Buckleton at 4, 281-86; Taylor at 517.

50. With reference to element (d) of claim 1, STRmix™ is used to perform a method that includes the step of “assuming a genotype value which is stored in a nontransient memory.” *See, e.g.*, Buckleton at Fig. 9.10; Taylor at 518.

51. With reference to element (e) of claim 1, STRmix™ is used to perform a method that includes the step of “deriving with a computer a variance of the amplification.” *See, e.g.*, Buckleton at 293; Taylor at 519.

52. With reference to element (f) of claim 1, STRmix™ is used to perform a method that includes the step of “determining a likelihood using a computer in communication with the memory, where the likelihood is defined as a probability of observing the generated data, and said probability depends on the genotype value and the variance.” *See, e.g.*, STRmix™ Operating Instructions at ¶¶ 3-4, 6.6-6.7; Buckleton at Fig. 9.11; Taylor at 517, 519.

53. The foregoing element-by-element comparison demonstrates that use of the accused STRmix™ probabilistic genotyping software product on suitable biological input data literally satisfies each and every element of at least claim 1 of the '642 Patent, thus literally infringing the patent. To the extent any element of claim 1 is deemed not to be literally satisfied, use of STRmix™ would nevertheless still infringe under the doctrine of equivalents because any differences between the claimed invention and the method performed by the accused product are insubstantial.

54. On information and belief, ESR and NicheVision (as ESR's exclusive sales representative) sell and offer to sell the STRmix™ probabilistic genotyping software product to customers in this judicial district and elsewhere in the United States, including numerous state and local law enforcement agencies and forensics laboratories.

55. The STRmix™ probabilistic genotyping software product constitutes a material part of the invention recited in claim 1 of the '642 Patent, being programmed to cause a material and substantial portion of the recited method steps to be performed, and it is not a staple article or commodity of commerce suitable for substantial non-infringing use. Moreover, on information and belief, Defendants are aware of the '642 Patent at least as a result of communications and interactions between Dr. Mark Perlin, the named inventor on the Patents-in-Suit and a co-founder of Cybergenetics, and Dr. John Buckleton, one of the developers of STRmix™ and a Principal Scientist at ESR. Consequently, Defendants know that the STRmix™ probabilistic genotyping software product is especially made or especially adapted for use in a manner that infringes the '642 Patent. Accordingly, Defendants' sale of the STRmix™ probabilistic genotyping software product contributes to infringement of the '642 Patent by their customers in violation of 35 U.S.C. § 271(c).

56. On information and belief, both by configuring the STRmix™ probabilistic genotyping software product to operate in a manner that Defendants know infringes the '642 Patent and by encouraging customers to use the STRmix™ probabilistic genotyping software product in a manner that Defendants know infringes the '642 Patent through training, product literature and customer support, Defendants are inducing infringement of the '642 Patent by their customers in violation of 35 U.S.C. § 271(b).

57. Defendants' infringement of the '642 Patent has caused Cybergenetics to suffer substantial monetary harm, including lost profits and price erosion relating to Cybergenetics' sale of competing products and services in the same markets served by Defendants.

58. The '642 Patent includes only method claims, and therefore the notice requirements of 35 U.S.C. § 287(a) are inapplicable. Cybergenetics is thus entitled to collect damages for any infringement of the '642 Patent by Defendants occurring up to six (6) years prior to the filing of this complaint in accordance with 35 U.S.C. § 286.

59. Defendants' infringement of the '642 Patent has caused and will continue to cause irreparable harm to Cybergenetics for which there is no adequate remedy at law, including but not limited to lost market share and lost goodwill that Cybergenetics would otherwise garner as the recognized innovator and sole authorized source of supply for probabilistic genotyping software configured to practice the methods covered by the '642 Patent.

60. On information and belief, Defendants' infringement of the '642 Patent has been willful, done deliberately and with full knowledge that the sale, offer to sell and use of the STRmix™ probabilistic genotyping software product infringes the '642 Patent, and without any reasonable, good-faith belief that the '642 Patent is invalid and/or not infringed, thereby

justifying an increase in the damages to be awarded Cybergenetics by up to three times the amount found or assessed, in accordance with 35 U.S.C. § 284.

61. Defendants' willful infringement of the '642 Patent renders this an exceptional case within the meaning of 35 U.S.C. § 285, justifying an award to Cybergenetics of its reasonable attorney fees incurred in connection with this litigation.

PRAYER FOR RELIEF

WHEREFORE, Cybergenetics prays for a judgment in its favor granting the following relief:

A. A finding that ESR and NicheVision have infringed the '021 and '642 Patents, holding them jointly and severally liable for such infringement;

B. A permanent injunction barring ESR and NicheVision, and all persons acting in concert with them, from infringing the '021 and '642 Patents;

C. An award of monetary damages pursuant to 35 U.S.C. § 284 in an amount adequate to compensate Cybergenetics for ESR's and NicheVision's infringement of the '021 and '642 Patents;

D. An order requiring ESR and NicheVision to pay Cybergenetics supplemental damages for any continuing post-verdict infringement up until entry of the final judgment, with an accounting, as needed;

E. A finding that ESR's and NicheVision's infringement of the '021 and '642 Patents has been willful;

F. An increase in the damages awarded to Cybergenetics up to three times the amount found by the jury or assessed by the Court, pursuant to 35 U.S.C. § 284;

G. A finding that this is an exceptional case within the meaning of 35 U.S.C. § 285, and a corresponding award of Cybergenetics' reasonable attorney fees incurred in connection

with this litigation;

H. An award of pre-judgment interest, post-judgment interest and costs, in amounts to be fixed by the Court; and

I. Any additional and further relief the Court deems just and proper.

JURY DEMAND

Pursuant to Federal Rule of Civil Procedure 38(b), Cybergenetics hereby demands a trial by jury on all issues so triable.

Dated: May 24, 2019

/s/ Michael J. Garvin

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